

F-Hamuel

1646

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/037,657A

DATE: 09/03/1999
TIME: 14:40:16

Input Set: I037657A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Hilton, Douglas J.
2 Nicola, Nicos A.
3 Farley, Alison
4 Wilson, Tracy
5 Zhang, Jian-Guo
6 Alexander, Warren
7 Rakar, Steven
8 Fabri, Louis
9 Kojima, Tetsuo
10 Maeda, Masatsugu
11 Kikuchi, Yasufumi
12 Nash, Andrew
13 <120> TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES
14 ENCODING SAME
15 <130> FILE REFERENCE: DAVIES COLLISON CAVE (CIP)
16 <140> CURRENT APPLICATION NUMBER: US/09/037,657A
17 <141> CURRENT FILING DATE: 1998-03-10
18 <150> EARLIER APPLICATION NUMBER: 08/928,720
19 <151> EARLIER FILING DATE: 1997-09-11
20 <160> NUMBER OF SEQ ID NOS: 54
21 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO 1
23 <211> LENGTH: 5
24 <212> TYPE: PRT
25 <213> ORGANISM: Unknown
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Unknown Organism: haemopoietin receptor
28 <220> FEATURE:
29 <221> NAME/KEY: UNSURE
30 <222> LOCATION: (3)
31 <223> OTHER INFORMATION: Unsure at position 3
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33 1 5
34 <210> SEQ ID NO 2
35 <211> LENGTH: 24
36 <212> TYPE: DNA
37 <213> ORGANISM: Artificial Sequence
38 <220> FEATURE:
39 <223> OTHER INFORMATION: Description of Artificial Sequence: M116 probe
40 <400> SEQUENCE: 2
41 actcgctcca gattcccgcc tttt
42 <210> SEQ ID NO 3
43 <211> LENGTH: 24

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45 <212> TYPE: DNA
46 <213> ORGANISM: Artificial Sequence
47 <220> FEATURE:
48 <223> OTHER INFORMATION: Description of Artificial Sequence:M108 probe
49 <400> SEQUENCE: 3
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51 <210> SEQ ID NO 4
52 <211> LENGTH: 24
53 <212> TYPE: DNA
54 <213> ORGANISM: Artificial Sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: Description of Artificial Sequence:M159 probe
57 <400> SEQUENCE: 4
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59 <210> SEQ ID NO 5
60 <211> LENGTH: 24
61 <212> TYPE: DNA
62 <213> ORGANISM: Artificial Sequence
63 <220> FEATURE:
64 <223> OTHER INFORMATION: Description of Artificial Sequence:M242 probe
65 <400> SEQUENCE: 5
66 cggctcacgt gcacgtcggg tggg 24
67 <210> SEQ ID NO 6
68 <211> LENGTH: 22
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial Sequence
71 <220> FEATURE:
72 <223> OTHER INFORMATION: Description of Artificial Sequence:M112 probe
73 <400> SEQUENCE: 6
74 agctgctgtt aaagggttc tc 22
75 <210> SEQ ID NO 7
76 <211> LENGTH: 15
77 <212> TYPE: DNA
78 <213> ORGANISM: Unknown
79 <220> FEATURE:
80 <223> OTHER INFORMATION: Description of Unknown Organism:Unsure
81 <220> FEATURE:
82 <221> NAME/KEY: unsure
83 <222> LOCATION: (1)
84 <223> OTHER INFORMATION: Unsure at position 1
85 <220> FEATURE:
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87 <222> LOCATION: (7)
88 <223> OTHER INFORMATION: Unsure at position 7
89 <220> FEATURE:
90 <221> NAME/KEY: unsure
91 <222> LOCATION: (10)
92 <223> OTHER INFORMATION: Unsure at position 10
93 <400> SEQUENCE: 7
94 rctccartcr ctcca 15

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RAW SEQUENCE LISTING
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95 <210> SEQ ID NO 8
96 <211> LENGTH: 15
97 <212> TYPE: DNA
98 <213> ORGANISM: Unknown
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Description of Unknown Organism:Unsure
101 <220> FEATURE:
102 <221> NAME/KEY: unsure
103 <222> LOCATION: (1)
104 <223> OTHER INFORMATION: Unsure at position 1
105 <220> FEATURE:
106 <221> NAME/KEY: unsure
107 <222> LOCATION: (7)
108 <223> OTHER INFORMATION: Unsure at position 7
109 <220> FEATURE:
110 <221> NAME/KEY: unsure
111 <222> LOCATION: (10)
112 <223> OTHER INFORMATION: Unsure at position 10
113 <400> SEQUENCE: 8
114 rctccaytcr ctcca 15
115 <210> SEQ ID NO 9
116 <211> LENGTH: 21
117 <212> TYPE: DNA
118 <213> ORGANISM: Artificial Sequence
119 <220> FEATURE:
120 <223> OTHER INFORMATION: Description of Artificial Sequence:1944 probe
121 <400> SEQUENCE: 9
122 aagtgtgacc atcatgtgga c 21
123 <210> SEQ ID NO 10
124 <211> LENGTH: 18
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Description of Artificial Sequence:2106 probe
129 <400> SEQUENCE: 10
130 ggaggtgtta aggaggcg 18
131 <210> SEQ ID NO 11
132 <211> LENGTH: 18
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Description of Artificial Sequence:2120 probe
137 <400> SEQUENCE: 11
138 atgcccgcgg gtcgcccc 18
139 <210> SEQ ID NO 12
140 <211> LENGTH: 1629
141 <212> TYPE: DNA
142 <213> ORGANISM: Unknown
143 <220> FEATURE:
144 <221> NAME/KEY: CDS

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RAW SEQUENCE LISTING
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145 <222> LOCATION: (124)..(1362)
 146 <220> FEATURE:
 147 <223> OTHER INFORMATION: Description of Unknown Organism:Murine NR6.1
 148 <400> SEQUENCE: 12
 149 ggcacgagct tcgctgtccg cgcccagtga cgcgcgtgcg gacccgagcc ccaatctgca 60
 150 ccccgccagac tcgccccccgc cccataccgg cgttgcagtc accgcccgtt gcgcgccacc 120
 151 ccc atg ccc gcg ggt cgc ccc ggc ccc gtc gcc caa tcc gcg cgg cgg 168
 Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
 152 1 5 10 15
 153 ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc 216
 154 Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Cys Val
 155 20 25 30
 156 ctc ggg gtg cct cgg ggc gga tcg gga gcc cac aca gct gta atc agc 264
 157 Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser
 158 35 40 45
 159 ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc 312
 160 Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
 161 50 55 60
 162 tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg 360
 163 Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
 164 65 70 75
 165 acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac 408
 166 Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn
 167 80 85 90 95
 168 acc tcc acc ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag 456
 169 Thr Ser Thr Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
 170 100 105 110
 171 cag tca gga gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg 504
 172 Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
 173 115 120 125
 174 gct ggc tcc tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac 552
 175 Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn
 176 130 135 140
 177 atc agc tgc tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca 600
 178 Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
 179 145 150 155
 180 ccg ggt gca cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag 648
 181 Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
 182 160 165 170 175
 183 tac aag ctg agg tgg tac ggt cag gat aac aca tgt gag gag tac cac 696
 184 Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
 185 180 185 190
 186 act gtg ggc cct cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc 744
 187 Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
 188 195 200 205
 189 act ccc tat gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca 792
 190 Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
 191 210 215 220
 192 aga tct gat gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac 840
 193 Arg Ser Asp Val Leu Thr Leu Asp Val Val Val Thr Thr Asp
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RAW SEQUENCE LISTING
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195	225	230	235	
196	ccc cca ccc gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag			888
197	Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln			
198	240	245	250	255
199	ctg agt gtg cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc			936
200	Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe			
201	260	265	270	
202	caa gcc aag tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg			984
203	Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp			
204	275	280	285	
205	aag gtg gtg gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc			1032
206	Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly			
207	290	295	300	
208	ctg aag ccc ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc			1080
209	Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe			
210	305	310	315	
211	ggg atc tat ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac			1128
212	Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His			
213	320	325	330	335
214	ccc acc gct gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc			1176
215	Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly			
216	340	345	350	
217	ggg gtg tgc gag ccg cgg ggc gag ccc agc tcg ggc ccg gtg cgg			1224
218	Gly Val Cys Glu Pro Arg Gly Glu Pro Ser Ser Gly Pro Val Arg			
219	355	360	365	
220	cgc gag ctc aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc			1272
221	Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys			
222	370	375	380	
223	tcg aac ctt agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag			1320
224	Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln			
225	385	390	395	
226	aag tca cac aag acc cga aac cag gtc ctg ccg gct aaa ctc			1362
227	Lys Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu			
228	400	405	410	
229	taaggatagg ccatccctcct gctgggtcag acctggaggc tcacctgaat tggagccct			1422
230	ctgtaccatc tggcaacaa agaaacctac cagaggctgg ggcacaatga gctcccacaa			1482
231	ccacagcttt ggtcccacatg atggtcacac ttggatatac cccagtgtgg gtaaggttgg			1542
232	ggtattgcag ggcctcccaa caatctctt aaataaaataa aggagttgtt caggtaaaaa			1602
233	aaaaaaaaaaaa aaaaaaaaaa aaaaaaaa			1629
234	<210> SEQ ID NO 13			
235	<211> LENGTH: 413			
236	<212> TYPE: PRT			
237	<213> ORGANISM: Unknown			
238	<220> FEATURE:			
239	<223> OTHER INFORMATION: Description of Unknown Organism: Murine NR6.1			
240	<400> SEQUENCE: 13			
241	Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro			
242	1	5	10	15
243	Pro Arg Pro Leu Ser Ser Leu Trp, Ser Pro Leu Leu Leu Cys Val Leu			
244	20	25	30	

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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**VERIFICATION SUMMARY
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DATE: 09/03/1999

TIME: 14:40:16

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Line ? Error/Warning

Original Text

33 W "N" or "Xaa" used: Feature required
1032 W "N" or "Xaa" used: Feature required
1036 W "N" or "Xaa" used: Feature required
1038 W "N" or "Xaa" used: Feature required

Trp Ser Xaa Trp Ser
Leu Arg Leu Val Arg Ser Glu Xaa His Met X
Leu Xaa Asp Leu Gly Gly Ser His Gln Ser P
Xaa Cys Pro His Thr Gly Cys Pro Gly Arg